

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/582,779

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

<input type="checkbox"/> 1 Wrapped Nucleics	<p>The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".</p>
<input type="checkbox"/> 2 Wrapped Aminos	<p>The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".</p>
<input type="checkbox"/> 3 Incorrect Line Length	<p>The rules require that a line not exceed 72 characters in length. This includes spaces.</p>
<input type="checkbox"/> 4 Misaligned Amino Acid Numbering	<p>The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.</p>
<input type="checkbox"/> 5 Non-ASCII	<p>This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.</p>
<input type="checkbox"/> 6 Variable Length	<p>Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.</p>
<input type="checkbox"/> 7 PatentIn ver. 2.0 "bug"	<p>A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.</p>
<input type="checkbox"/> 8 Skipped Sequences (OLD RULES)	<p>Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). </p>
<input type="checkbox"/> 9 Skipped Sequences (NEW RULES)	<p>Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000 </p>
<input checked="" type="checkbox"/> 10 Use of n's or Xaa's (NEW RULES)	<p>Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.</p>
<input type="checkbox"/> 11 Use of <213>Organism (NEW RULES)	<p>Sequence(s) _____ are missing this mandatory field or its response. 3-6 </p>
<input checked="" type="checkbox"/> 12 Use of <220>Feature (NEW RULES)	<p>Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)</p>
<input type="checkbox"/> 13 PatentIn ver. 2.0 "bug"	<p>Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.</p>

N-mu
1636

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/582,779

DATE: 01/29/2001
TIME: 16:26:49

Input Set : A:\ES.txt
Output Set: N:\CRF3\01292001\I582779.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Pompejus, Markus
4 Doval, Jose Luis Revuelta
5 Garcia, Maria Angeles Santos
7 <120> TITLE OF INVENTION: Orotidine-5'-phosphate decarboxylase gene, gene construct comprising
8 this gene and its use.
OK 0 <130> FILE REFERENCE:
10 <140> CURRENT APPLICATION NUMBER: US 09/582,779
11 <141> CURRENT FILING DATE: 2000-07-03
13 <150> PRIOR APPLICATION NUMBER: Germany/19801120.2
14 <151> PRIOR FILING DATE: 1998-01-15
E--> 16 <160> NUMBER OF SEQ ID NOS: 5
18 <170> SOFTWARE: WordPerfect version 6.1

⑥ (next page)

ERRORED SEQUENCES

180 <210> SEQ ID NO: 3
181 <211> LENGTH: 18
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial sequence
185 <220> FEATURE:
186 <221> NAME/KEY: misc_feature
187 <222> LOCATION: 1 ... 18
W--> 189 <223> OTHER INFORMATION:
189 <400> SEQUENCE: 3

E--> 191 ttttttttccayathtgty
194 <210> SEQ ID NO: 4
195 <211> LENGTH: 23
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial sequence
199 <220> FEATURE:
200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: 1 ... 23
W--> 203 <223> OTHER INFORMATION:
203 <400> SEQUENCE: 4

E--> 205 taytgtytgc cmarytttgc ncc
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 26
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial sequence
213 <220> FEATURE:
214 <221> NAME/KEY: misc_feature
215 <222> LOCATION: 1 ... 26
W--> 217 <223> OTHER INFORMATION:
217 <400> SEQUENCE: 5

E--> 219 tttytthattt tygargaymg naartt
222 <210> SEQ ID NO: 6

Global error

see item 12 on

Error summary sheet

*18 <insert cumulative base total at right margin
of each line*

same error as above

see item 10 on

Error summary

sheet regarding

n's

total

*same
error*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/582,779

DATE: 01/29/2001
TIME: 16:26:50

Input Set : A:\ES.txt
Output Set: N:\CRF3\01292001\I582779.raw

223 <211> LENGTH: 19
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial sequence
227 <220> FEATURE:
228 <221> NAME/KEY: misc_feature
229 <222> LOCATION: 1 ... 19
W--> 231 <223> OTHER INFORMATION:
231 <400> SEQUENCE: 6
E--> 233 gcaaaaaa rhamnose ✓ total

last sequence

Suggestion: Consult new sequence
Rules for valid format

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/582,779

DATE: 01/29/2001

TIME: 16:26:51

Input Set : A:\ES.txt

Output Set: N:\CRF3\01292001\I582779.raw

L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:189 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:191 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:3
L:203 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:205 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:4
L:217 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:219 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:5
L:231 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:233 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:6
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (5) Counted (6)